RAW SEQUENCE LISTING

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Application Serial Number: 09/774,681C

Source: 1FW/6

Date Processed by STIC: 07-19-2005

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PATENT APPLICATION: US/09/774,681C   TIME: 11:23:13

Input Set : A:\48355793.app
Output Set: N:\CRF4\07192005\I774681C.raw

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 3 <110> APPLICANT: SHERMAN, LINDA A.
 4         LUSTGARTEN, JOSEPH
 6 <120> TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
 7         SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
 9 <130> FILE REFERENCE: 48340/55793-DIV
11 <140> CURRENT APPLICATION NUMBER: 09/774,681C
12 <141> CURRENT FILING DATE: 2001-02-01
14 <150> PRIOR APPLICATION NUMBER: 08/812,393
15 <151> PRIOR FILING DATE: 1997-03-05
17 <150> PRIOR APPLICATION NUMBER: 60/012,845
18 <151> PRIOR FILING DATE: 1996-03-05
20 <160> NUMBER OF SEQ ID NOS: 65
22 <170> SOFTWARE: PatentIn Ver. 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1350
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1332)
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
35         single chain TCR derivative nucleotide sequence
37 <400> SEQUENCE: 1
38 ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg    48
39 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
40   1               5                  10                  15
42 cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc    96
43 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
44             20                  25                  30
46 ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc   144
47 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
48         35                  40                  45
50 atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga   192
51 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
52     50                  55                  60
54 ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga   240
55 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
56  65                  70                  75                  80
58 ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att   288
59 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
60             85                  90                  95
62 tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat   336
```

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63  Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
64               100             105                 110
66  tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc   384
67  Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
68           115             120                 125
70  tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt   432
71  Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
72       130             135                 140
74  gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca   480
75  Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
76  145             150                 155                 160
78  gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac   528
79  Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
80               165             170                 175
82  aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg   576
83  Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
84               180             185                 190
86  atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct   624
87  Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
88           195             200                 205
90  gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att   672
91  Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
92       210             215                 220
94  ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc   720
95  Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
96  225             230                 235                 240
98  ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag   768
99  Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
100              245             250                 255
102 ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg   816
103 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
104              260             265                 270
106 ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca   864
107 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
108          275             280                 285
110 cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca   912
111 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
112      290             295                 300
114 tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc   960
115 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
116 305             310                 315                 320
118 ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc   1008
119 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
120              325             330                 335
122 agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc   1056
123 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
124              340             345                 350
126 tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac   1104
127 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
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128        355                    360                    365
130 aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag   1152
131 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
132        370                    375                    380
134 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg   1200
135 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
136 385                    390                    395                    400
138 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag   1248
139 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
140         .              405                    410                    415
142 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc   1296
143 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
144        420                    425                    430
146 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc   1344
147 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
148        435                    440
150 acc gcg                                                            1350
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 444
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
160        single chain TCR protein
162 <400> SEQUENCE: 2
163 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
164 1               5                   10                  15
166 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
167             20                  25                  30
169 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
170         35                  40                  45
172 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
173     50                  55                  60
175 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
176 65                  70                  75                  80
178 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
179                 85                  90                  95
181 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
182             100                 105                 110
184 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
185         115                 120                 125
187 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
188     130                 135                 140
190 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
191 145                 150                 155                 160
193 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
194                 165                 170                 175
196 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
197             180                 185                 190
```

```
199 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
200         195                 200                 205
202 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
203         210                 215                 220
205 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
206 225                 230                 235                 240
208 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
209                 245                 250                 255
211 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
212                 260                 265                 270
214 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
215         275                 280                 285
217 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
218         290                 295                 300
220 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
221 305                 310                 315                 320
223 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
224                 325                 330                 335
226 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
227         340                 345                 350
229 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
230         355                 360                 365
232 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
233         370                 375                 380
235 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
236 385                 390                 395                 400
238 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
239                 405                 410                 415
241 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
242         420                 425                 430
244 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
245         435                 440
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 24
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
256 <400> SEQUENCE: 3
257 cccaaggcac tgatgttcat cttc                                      24
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 27
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
268 <400> SEQUENCE: 4
269 tgagacaaag tccccaatct ctgacag                                   27
272 <210> SEQ ID NO: 5
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273 <211> LENGTH: 26
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
280 <400> SEQUENCE: 5
281 ctgcagctgc tcctcaagta ctattc                                26
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 28
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
292 <400> SEQUENCE: 6
293 tcccggagaa ggtccacagt tcctctttt                              28
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 29
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
304 <400> SEQUENCE: 7
305 gaagcagcag agggtttgaa gccacatac                              29
308 <210> SEQ ID NO: 8
309 <211> LENGTH: 27
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
316 <400> SEQUENCE: 8
317 ggcaggtctt cagttgctta tgaaggt                                27
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 27
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
328 <400> SEQUENCE: 9
329 ggttcctctt cagggtccag aatatgt                                27
332 <210> SEQ ID NO: 10
333 <211> LENGTH: 27
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
340 <400> SEQUENCE: 10
341 gcgaagaact caccctggac tgttcat                                27
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 30
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/19/2005
PATENT APPLICATION: **US/09/774,681C**   TIME: 11:23:14

Input Set : **A:\48355793.app**
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<u>**Invalid Line Length:**</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 245

VERIFICATION SUMMARY   DATE: 07/19/2005
PATENT APPLICATION: US/09/774,681C   TIME: 11:23:14

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